

Om protein - protein search, using sw model

Run on: June 7, 2001, 00:18:23 ; Search time 28.04 Seconds
 (without alignments)
 924.800 Million cell updates/sec

title: US-09-494-297-2
 Perfect score: 3945
 Sequence: 1 MKKTRFPNKLNTLNTQVRLS..... IAGISLIGIWGHTIRIKHD 757

Scoring table: BLOSUM62
 Gapext 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0
 Maximum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : SwissProt_39;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					
Result No.	Score	Query Match	Length	DB ID	Description
1	148	3.8	1183	1 CNA_STAU	053654 staphylococ
2	139	3.5	621	1 HTPG_HELPY	P56116 helicobacte
3	139	3.5	1433	1 SUBE_BACSU	P16397 bacillus su
4	139	3.5	2366	1 TOBR_CLODI	P18177 clostridium
5	137	3.5	1177	1 Y3071_MYCGE	P47419 mycoplasma
6	136.5	3.5	4590	1 FATH_HUMAN	014519 homo sapien
7	135	3.4	1176	1 SLAP_BACSH	P36537 bacillus sp
8	135	3.4	1228	1 SLAB_BACST	P35825 bacillus st
9	135	3.4	1301	1 SAC3_YEAST	P46674 saccharomy
10	132.5	3.4	1116	1 SLPH_BACBR	P38538 bacillus br
11	132.5	3.4	3097	1 CADN_DROME	015943 drosophila
12	130.5	3.3	881	1 LHS1_YEAST	P36016 saccharomy
13	130.5	3.3	908	1 DPOB_BORBU	051498 borrelia bu
14	130	3.3	621	1 HTPG_HELPJ	Q9zum2 helicobacte
15	130	3.3	1372	1 FUSL_SCHPO	010719 schizophec
16	129	3.3	461	1 P55G_HUMAN	Q92569 homo sapien
17	129	3.3	1292	1 RPPG_MYCGE	P47582 mycoplasma
18	128.5	3.3	914	1 PBPX_BACSU	P39793 bacillus su
19	128.5	3.3	1828	1 MAP2_MOUSE	P20357 mus musculu
20	128	3.2	1375	1 GTFG_STRMU	P13470 streptococc
21	128	3.2	1394	1 HAP_HAEIN	P45387 haemophilus
22	127	3.2	984	1 HYSA_STRAZ	Q53391 streptococc
23	127	3.2	1651	1 VITG_CAEEL	P18948 caenorhabdi
24	126.5	3.2	822	1 DEXT_STRSL	Q59912 streptococc
25	126.5	3.2	1772	1 MSP1_PLAVO	P13228 plasmodium
26	126	3.2	1036	1 Y414_MYCGE	P47653 mycoplasma
27	126	3.2	1409	1 HAPL_HAEIN	P44596 haemophilus
28	125	3.2	700	1 HSPC_DC07	P54651 dictyostelli
29	125	3.2	968	1 CC28_SCHPO	Q17752 schizosacch
30	124.5	3.2	461	1 P556_BOVIN	Q046404 bos tauru
31	124.5	3.2	1251	1 RBP2_PLAVB	Q00799 plasmodium
32	124	3.2	6359	1 BAC2_BACLI	Q68008 bacillus
33	3.1	2334	1 WAPB_BACSU	Q07853 bacillus su	

ALIGNMENTS					
RESULT	1	CNA_STRAU	STANDARD;	PRT;	1183 AA.
ID	CNA_STRAU				
AC	053654;				
DT	15-DEC-1998 (Rel. 37, Created)				
DT	15-DEC-1998 (Rel. 37, Last sequence update)				
DE	COLLAGEN ADHESIN PRECURSOR.				
GN	CNA.				
OS	Staphylococcus aureus.				
OC	Bacteria; Firmicutes; Bacillus/Clostridium group;				
OC	Bacillus/Staphylococcus group; Staphylococcus.				
OX	NCBI_TaxID=1280;				
RN	[1]				
RP	SEQUENCE FROM N. A.				
RC	STRAIN=FDA 574;				
RX	MEDLINE=92165839; PUBMED=1311320;				
RA	Patti J.M., Jonsson H., Guss B., Switalski L.M., Wiberg K.,				
RA	Lindberg M., Hoeook M.,				
RT	"Molecular characterization and expression of a gene encoding a				
RT	Staphylococcus aureus collagen adhesin.";				
RL	J. Biol. Chem. 267:4766-4772(1992).				
RN	[2]				
RP	ERRATUM.				
RA	Patti J.M., Jonsson H., Guss B., Switalski L.M., Wiberg K.,				
RL	Lindberg M., Hoeook M.,				
RN	J. Biol. Chem. 269:11672-11672(1994).				
[3]					
RP	COLLAGEN-BINDING DOMAIN.				
RC	STRAIN=FDA 574;				
RX	MEDLINE=94032261; PUBMED=8218209;				
RA	Patti J.M., Boiles J.C., Hoeook M.,				
RT	"Identification and biochemical characterization of the ligand				
RT	binding domain of the collagen adhesin from Staphylococcus aureus.;"				
RL	Biochemistry 32:11428-11435(1993).				
RN	[4]				
RP	X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 169-318.				
RX	MEDLINE=97475225; PUBMED=9334749;				
RA	Symersky J., Patti J.M., Carson M., House-Pompeo K., Teale M.,				
RA	Moore D., Jin L., Schneider A., DeLucas L.J., Hoeook M.,				
RA	Narayana S.V.L.				
RT	"Structure of the collagen-binding domain from a Staphylococcus				
RT	aureus adhesin."				
RL	Nat. Struct. Biol. 4:833-838(1997).				
CC	-I- FUNCTION: MEDIATES ATTACHMENT OF STAPHYLOCCAL CELLS TO				
CC	COLLAGEN-CONTAINING SUBSTRATA.				
CC	-I- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. CELL WALL.				
CC	-I- SIMILARITY: TO OTHER STREPTOCOCAL AND STAPHYLOCCAL PROTEINS				
CC	IN THE REGION OF THE MEMBRANE ANCHOR.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
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CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/				

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CC	773 LPKVDEGKKI-----BYTVI-----EDRVKDVITDINGTITNKYPTETSATVTKW 820
DR	644 -DKTNLE-----FKDGKAT-----INLKIGESLTIQGLE-----GYSVYKE- 680
DR	PDB: 1AMX; 24-JUN-98.
DR	INTERPRO: IPR001899; -.
DR	PROSITE: PS00343; GRAM_POS_ANCHORING: FALSE_NEG.
KW	Signal; Repeat; Transmembrane; Cell wall; 3D-structure.
FT	1 29
FT	SIGNAL
FT	1183 30
FT	CHATIN
FT	1157 30
FT	DOMAIN
FT	1177 1158
FT	TRANSMEM
FT	1183 1178
FT	MEMBRANE
FT	1318 151
FT	ANCHOR
FT	1318 151
FT	CYTOSMATIC (POTENTIAL).
FT	COLLAGEN-BINDING.
FT	3 X 187 AA APPROXIMATE TANDEM REPEATS.
FT	DOMAIN 1093 1093
FT	DOMAIN 1157 1157
FT	DOMAIN 1156 1156
FT	LYS/PRO-RICH (CELL WALL-SPANNING).
FT	CONSERVED IN GRAM-POSITIVE COCCI SURFACE
FT	PROTEINS.
REPEAT	533 719
REPEAT	720 906
REPEAT	907 1093
SEQUENCE	1183 AA; 133066 MW; B6A1CC07E575D76 CRC64;
Query Match	3.8%; Score 148; DB 1; Length 1183;
Best Local Similarity	19.7%; Pred. No. 0.83; Length 1183;
Matches	165; Conservative 123; Mismatches 299; Indels 252; Gaps 44;
Qy	64 PDSSEYRWY---GYESVYRQHPIYK-----QFRVYAHDLRVNLESSRSY---QYCF 109
Qy	182 PDETTHVRFLNINNNEKSYVSQKDRITDKDQILOGQQLDLSITMNVGTHNSNTYSQGAI 241
Qy	110 NLKKATPLGS-----DSSVKKWYKKRDKISRFEDAMSFRITG----- 148
Qy	242 DFEKAPP-GSKITVDKTKNTIDTVIFOGYGSYNSFSINYK-----TITNEQQEKFNN 295
Qy	149 -----DELNOKURARVMMNGHPDONGIMEG-----LEPLNAIRYEQAEWYYSIDNA 194
Qy	296 QAWYQHKGKEVNGK--SFNHVHNINANAGIETVKGELVKLQDKDK 344
Qy	195 PISNPDESK REESNLVLSITSQLSLMRQLKQDIDNLTAKMVKQOPDDFQFQFSE- 252
Qy	345 PIAN- VKEFLSKKDGCVKQNO-----KELEIITDANGIANITALPKPSGDYIKEIAPR 397
Qy	253 ---DKGDY-----NKGQNLSSGGL-----VPTKPPTPGDPMPMPNQPORTSV 293
Qy	398 PYTFDRDKKEYFPTIMKTDNQGYFTTENAKATEKTKDVSQAKWEGIQKVKP-----TI 451
Db	394 LIRKVALGDS-----KLLERATLQLTGDNNTNSFOARWFSSND-IGRIELSDGT 342
Qy	294 YLTELN-----SPAGYSIE-----PI-TPKVEAGKVYTIDGKQIENPKIE 385
Qy	499 YLVKNAQAGDTPSFGKVKYKRENGLYVNTNEKPTIISIGKVWDDKDNQGKPEK- 556
Qy	386 VEPSYSEAYNDFEEFSVLTONYAKFV-----AKNKNSSSOVYCFNADLKSPPDBDG 440
Db	452 YFKLYQDDNNTTPVKAIEKRLDGTIVKWSNL-----PENDINGKAIR----- 498
Qy	343 YLTELN-----SPAGYSIE-----PI-TPKVEAGKVYTIDGKQIENPKIE 385
Db	557 --VSVNLLANGEKVKLTDVSETNWKYEFKDLPKIPEG-KKIEYTQEDHVKDITDIN 612
Qy	441 GKTMTDPFTGEVKYHIAGRDLFVKVVKPROTDPPFLKHKKVTK----- 488
Db	613 GTTITNRYKTPGETSATVTKNNDDNNODGKRPTETKVELYQDGKATGKTAI
Qy	613 LNESNNWTH 672
Qy	673 TWTGLDEKAGQKVYKTVELTKVKGYTHVNDMDGNLIVNKYTFETTSISGEKWD- 731
Qy	533 HGFGLMDNSTLAVAKILVEYQADSNPFDLDFITNNNKYVOSL--IGTQWHPEDLVD 589
Qy	732 ---DKDN-----QDGKRPKVSVN-LIADGEVKVLTIDVSETNWKYE-FKD 772
Db	590 IIRMEDKKEVIVPTVHNLTRKTVTGLAGDRKQDFHIE-----LKNKQELLSQTWKT- 643
Qy	644 -DKTNLE-----FKDGKAT-----INLKIGESLTIQGLE-----GYSVYKE- 680
Qy	1183 30
Db	821 DDNNHODGKRPTETKVELYQDGKATGKTAI
Qy	681 TDSEGCKVQNSQEAVANATVSK-----IGITSDTLEAFENKEVWPTQYDQK1--NG 731
Db	881 TKVQYTHVNDNGNGLVLTNKVPPETTSISGEKWDKNDQGKRPKVSVNLLANG 939
RESULT	2
HTPG_HELPY	HTPG_HELPY STANDARD; PRT; 621 AA.
ID	HTPG_HELPY STANDARD;
AC	P56116;
DT	01-NOV-1997 (Rel. 35, Created)
DT	01-NOV-1997 (Rel. 35, Last sequence update)
DT	01-NOV-1997 (Rel. 35, Last annotation update)
DE	HEAT SHOCK PROTEIN HTPG (HIGH TEMPERATURE PROTEIN G).
GN	HTPG OR HP0210.
OS	Helicobacter pylori (Campylobacter pylori)
OC	Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OX	Helicobacter.
NCBI_TaxID	210;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=26595 / ATCC 700392;
RX	MEDLINE:97394467; PUBMED=9252185;
RA	Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
RA	Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
RA	Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
RA	Lofthus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
RA	McKenney K., Fitzgerald L.M., Lee N., Khalak H.G., Hickie E.K.,
RA	Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
RA	Cotton M.D., Weidman J.M., Fuerst C., Bowman C., Watthey L., Wallin E.,
RA	Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
RA	Venter J.C.;
RT	"The complete genome sequence of the gastric pathogen Helicobacter pylori."
RL	Nature 380:539-547(1997).
CC	-!- FUNCTION: MOLECULAR CHAPERONE. HAS ATPASE ACTIVITY
CC	(BY SIMILARITY)
CC	-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 90 FAMILY
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation in
CC	the European Bioinformatics Institute. There are no restrictions on its
CC	use by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	EMBL: AE000541; AAD07278.1; -.
DR	Inter-Pro: IPR001404; -.
DR	Pfam: PF00183; HSP90; 1.
DR	PRINTS: PR00775; HEATSHOCK90.
DR	PROSITE: PS00288; HSP90; 1.
KW	Chaperone; ATP-binding; Heat shock; Sequence;
Qy	256 -DKV-----KGVNLSSGLVPTKRPPTGDPMPNQPTTSVLRKVAIGDY 303

RA	"Molecular cloning and tissue expression of FAT, the human homologue of the Drosophila fat gene that is located on chromosome 4q34-q35 and encodes a putative adhesion molecule.;"
RT	Genomics 30:1977-223(1995)
RL	-1- FUNCTION: COULD FUNCTION AS A CELL-ADHESION PROTEIN.
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
CC	-1- TISSUE SPECIFICITY: EXPRESSED IN MANY EPITHELIAL AND SOME ENDOTHELIAL AND SMOOTH MUSCLE CELLS.
CC	-1- SIMILARITY: BELONGS TO THE CADHERIN FAMILY OF CELL ADHESION MOLECULES. CONTAINS 34 CADHERIN TYPE REPEATS.
CC	-1- SIMILARITY: CONTAINS 5 EGF-LIKE DOMAINS.
CC	-1- SIMILARITY: CONTAINS 1 LAMINTIN G-LIKE REPEAT.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
EMBL; EMBL; HSSP; HSSP; P01132; 1EPH. MIN: 600976; -	
PR: P00028; laminin; 33. P00034; laminin; G; 1. P00055; CADHERIN. P00010; ASX_HIDROXVL; 1. P000232; CADHERIN; 16. P00022; EGF_1; 4. P00186; EGF_2; 1. P00187; EGF_CA; 1. PROSITE: PS00186; EGF_1; 4. PROSITE: PS00187; EGF_2; 1. PROSITE: PS00186; EGF_CA; 1.	
DR	Cell adhesion; Signal; Glycoprotein; Transmembrane; Calcium-binding; repeat; EGF-like domain.
DR	SIGNAL 1 21
DR	CHAIN 22 4590
DR	POTENTIAL. CADHERIN RELATED TUMOR SUPPRESSOR HOMOLOG.
FT	DOMAIN 22 4183 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 4184 4204 POTENTIAL.
FT	DOMAIN 4205 4590 CYTOPLASMIC (POTENTIAL).
FT	CADHERIN 1. 22 149 CADHERIN 2. 256 361 CADHERIN 3. CADHERIN 4. CADHERIN 5. CADHERIN 6. CADHERIN 7. CADHERIN 8. CADHERIN 9. CADHERIN 10. CADHERIN 11. CADHERIN 12. CADHERIN 13. CADHERIN 14. CADHERIN 15. CADHERIN 16. CADHERIN 17. CADHERIN 18. CADHERIN 19. CADHERIN 20. CADHERIN 21. CADHERIN 22. CADHERIN 23. CADHERIN 24. CADHERIN 25.
FT	DOMAIN 1563 1670 DOMAIN 1671 1759 DOMAIN 1770 1882 DOMAIN 1739 1883 DOMAIN 1983 2084 DOMAIN 2185 2286 DOMAIN 2287 2393 DOMAIN 2394 2495 DOMAIN 2496 2599 DOMAIN 2705
FT	DOMAIN 2706 2812 DOMAIN 2921 3024 DOMAIN 3025 3127 DOMAIN 3128 3232 DOMAIN 3233 3337 DOMAIN 3338 3442 DOMAIN 3443 3545 DOMAIN 3547 3649 DOMAIN 3790 3827 DOMAIN 3836 4004 DOMAIN 4013 4051 DOMAIN 4052 4089 DOMAIN 4090 4125 DOMAIN 4127 4163 DOMAIN 440 440 CARBOHYD 333 333 CARBOHYD 660 660 CARBOHYD 740 740 CARBOHYD 791 791 CARBOHYD 998 998 CARBOHYD 1426 1426 CARBOHYD 1551 1551 CARBOHYD 1751 1751 CARBOHYD 1867 1867 CARBOHYD 1905 1905 CARBOHYD 1943 1943 CARBOHYD 1994 1994 CARBOHYD 2328 2328 CARBOHYD 2467 2467 CARBOHYD 3326 3326 CARBOHYD 3424 3424 CARBOHYD 3446 3446 CARBOHYD 3615 3615 CARBOHYD 3642 3642 CARBOHYD 3718 3718 CARBOHYD 4154 4154
FT	4590 AA; 506273 MW; 0443CCD000E60A7 CRG64; SQ
FT	SEQUENCE
FT	Query Match 3.5%; Score 136.5; DB 1; Length 4590; Best Local Similarity 19.8%; Pred. No. 28; Mismatches 316; Indels 281; Gaps 46; Matches 176; Conservative 118; Mismatches 316; Indels 281; Gaps 46;
FT	Homolog: HOMOLOG.
FT	POTENTIAL.
FT	CYTOSOLIC (POTENTIAL).
FT	CADHERIN 1. 22 149 CADHERIN 2. 256 361 CADHERIN 3. CADHERIN 4. CADHERIN 5. CADHERIN 6. CADHERIN 7. CADHERIN 8. CADHERIN 9. CADHERIN 10. CADHERIN 11. CADHERIN 12. CADHERIN 13. CADHERIN 14. CADHERIN 15. CADHERIN 16. CADHERIN 17. CADHERIN 18. CADHERIN 19. CADHERIN 20. CADHERIN 21. CADHERIN 22. CADHERIN 23. CADHERIN 24. CADHERIN 25.
FT	47 AKTVFGLVESSTDNA--NPDSSESYRNGYE---SYVRGHPYKQFRVADLRLVNL 98
Db	2573 AKDAGKGKAFCTWNLVILTDNDNAPQFRATKVEVNGSAAKTSSWKSASAD----- 2626
Qy	99 ESSRSYQYTCF---NLUKKAFFLGLSDSVKVKYKHDGISTKEDYAMSPRITGDELNQ 153
Db	2627 EGSNADTVAEADSESVENKLEINKUSGVITRSLIGLENFTFF----- 2674
Qy	154 KLRAMVNGHQNANGM-----EGLER-----LNARIVQE 185
Db	2675 -VRAV-DNGSPSKESVWVVKLPPEMOLPKRSEPEVTFVSEDPVGTEDILIRAHIS 2732
Qy	186 AVWYSS--DNAPISNPDESKRKESESNLVT-----QLSLMRQALKLQIDPN 231
Db	2733 GTVLYSLVKGNPTEINRDESFVIDRQSGRKLEKSLDHETTKWQFQSLARCTQD-DHE 2790
Qy	232 LATKMPKQVPDFQLSFESEDQGDYKNG-----YONLISGLV-----PTKPPPG 279
Db	2791 MYASV-----DVSIOVKADNNSPVFSSPYAFTVNLPGSSRVIGRASDADGNG 2844
Qy	339 SDGTT--YTLTELNSPAGYSIAEPTIYKE-----AGKVYII-----DGKQIE 379
Db	2901 SSTAIVDVTVDVND-----SPRFTAEIYKGTVSEDDQPGVIALISTDADSEEL- 2952
Qy	380 NPKKEIWPYSVAYNDEEFSVLTQVAKFYVAKNKGSSQVYVCNADLKSPPDSE 439

FT	DOMAIN	973	1078	CADHERIN 7.
FT	DOMAIN	1087	1183	CADHERIN 8.
FT	DOMAIN	1193	1299	CADHERIN 9.
FT	DOMAIN	1307	1414	CADHERIN 10.
FT	DOMAIN	1423	1514	CADHERIN 11.
FT	DOMAIN	1523	1630	CADHERIN 12.
FT	DOMAIN	1639	1742	CADHERIN 13.
FT	DOMAIN	1749	1861	CADHERIN 14.
FT	DOMAIN	1870	1966	CADHERIN 15.
FT	DOMAIN	1974	2085	CADHERIN 16.
FT	DOMAIN	2345	2377	LAMININ G-LIKE 1.
FT	DOMAIN	2407	2585	LAMININ G-LIKE 2.
FT	DOMAIN	2592	2627	EGF-LIKE 3.
FT	DOMAIN	2869	2902	LAMININ G-LIKE 2.
FT	DISUFDID	2661	2822	POTENTIAL.
FT	DISUFDID	2351	2357	POTENTIAL.
FT	DISUFDID	2368	2377	POTENTIAL.
FT	DISUFDID	2396	2607	POTENTIAL.
FT	DISUFDID	2601	2616	POTENTIAL.
FT	DISUFDID	2618	2627	POTENTIAL.
FT	DISUFDID	2869	2880	POTENTIAL.
FT	DISUFDID	2874	2891	POTENTIAL.
FT	DISUFDID	2893	2902	POTENTIAL.
FT	CARBHYD	97	150	N-LINED (GLCNAC, . .) (POTENTIAL).
FT	CARBHYD	150	150	N-LINED (GLCNAC, . .) (POTENTIAL).
FT	CARBHYD	3225	3225	N-LINED (GLCNAC, . .) (POTENTIAL).
FT	CARBHYD	426	426	N-LINED (GLCNAC, . .) (POTENTIAL).
FT	CARBHYD	930	930	N-LINED (GLCNAC, . .) (POTENTIAL).
FT	CARBHYD	1266	1266	N-LINED (GLCNAC, . .) (POTENTIAL).
FT	VARIANT	1425	1425	E -> K (IN ALLELE CADN-M12; MUSCLE DEFECTS).
FT	CONFLICT	1342	1342	P -> A (IN REF. 1).
FT	CONFLICT	2785	2786	S -> T (IN REF. 1).
SO	SEQUENCE	3097	AA;	347201 MW; 082242F28D9B5CC3 CRC64;
Query	Match			3.4%; Score 132.5; DB 1; Length 3097;
Best	Local Similarity	19.8%	Score	DB 1; Length 3097;
Matches	114;	Conservative	89;	Pred. No. 26; Matches 192; Indels 181; Gaps 29;
Qy	287	OPQQTTSVLLKRYA-IGDYSKLLLEGATLQLQT--GDNNSRQARVFSSNDTGERIELSDGTV	343	343
Db	719	OPHQVSLIVATEDSGGFSTSVD-LTIRVTDVNDWAPKFELPDYQAHNVDEDIPLGTSIL	777	777
Qy	344	TTEILNSPAG----YSTAEPIKTVKEAGKVYTIDKGKQIENPKKEIVPYSVEAYNDP	397	397
Db	778	RVKAMDSDSQNSAEEYELVSDD-HFADWSNGI--IIVNNKQDADNNNAYEYFIVIAKDG	834	834
Qy	398	E--EFSVLTQNYAKFYAKNKNGS--SQWVTCFNADIKSPP-----DSED	439	439
Db	835	EPPKSCVATR----VYTKNKNDDEPKFSSQQVTPNVDNAPNTLVTWASDKGDN	889	889
Qy	440	-----GGKMTMPDT----TGEVRYTHA--GDLDEKTY-----	468	468
Db	890	VRFGVFGGGTSQQFVIEDTGVILHNAKISLDKQYKEVLTNTAMDGSCVNGDQTIH	949	949
Qy	469	-----KPRDTPDPFLKHK-----KVI---EKGYREKQAIER	499	499
Db	950	STAVWVFITDVNDKPVFIFCSTVYPKVREGAPNGSPVYKWADEDKSY--NGQ--VKY	1005	1005
Qy	500	SGLTENPVLRAATQALAYYFDSAEELDKDKLKYHG-----FGDMDNSTL-AVAK	547	547
Db	1007	S-IVQOPNQGKTFKTV--DEBTIGEVSTNKYFDRGGDDKGKVSVTVKATDQGDPSPLEGVC	1063	1063
Qy	548	ILVEYAQDSNPQQLDLDFTIPNNKKYQSIQTMHPEDJVDITMEDKKEVIVPTHNL	607	607
Db	1064	FTVEITDVNDNPPPLFDQKTY-ENVQDASIGT-----NILRVS-----	1101	1101
Qy	608	LRKTVIGLAGDTKPFHETELKNNKKQELISQTVKUTDKTNEFKDGGKTVFVSVTVKATDQGDPSPLEGVC	667	667
Db	1102	-----ASDEDAD-----NNGAIIVSLLTAPFPNPNDLVEFQIA-----	1133	1133
FT	RESULT	12		
	LHS1_YEAST			
ID	LHS1_YEAST			
AC	P36016;			
DT	01-JUN-1994 (Rel. 29, Created)			
DT	01-JUN-1994 (Rel. 29, Last sequence update)			
DT	01-NOV-1997 (Rel. 35, Last annotation update)			
DE	HEAT SHOCK PROTEIN 70 HOMOLOG LHS1 PRECURSOR.			
GN	LHS1 OR YK073W OR YKL355.			
OC	Saccharomyces cerevisiae (Baker's yeast),			
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;			
OC	Saccharomyetales; Saccharomycetaceae; Saccharomyces;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Pohl T M, Pohl F M;			
RL	Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.			
RA	Craven R.A., Egerton M., Stirling C.J.;			
RT	"A novel Hsp70 of the yeast ER lumen is required for the efficient translocation of a number of protein precursors."			
RL	EMBO J. 15:2640-2650(1996).			
CC	-- FUNCTION: PROBABLY ACTS AS A CHAPERONE INVOLVED IN BOTH POLYPEPTIDE TRANSLOCATION AND SUBSEQUENT FOLDING.			
CC	-- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.			
CC	-- PTM: N-GLYCOSYLATED.			
CC	-- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation of the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	EMBL; X75700; CAA53401.1; -.			
DR	Z28073; CAA81910.1; -.			
DR	EMBL; P37895; S37895.			
DR	PIR; S39169; S39169.			
DR	S44514; S44514.			
DR	SCD; S0001556; LHS1.			
DR	InterPro; IPR000886; -.			
DR	InterPro; IPR001023; -.			
DR	PROSITE; PS00014; ER-TARGET; 1.			
DR	PROSITE; PS00329; HSP70-2; 1.			
DR	PROSITE; PS01036; HSP70-3; 1.			
DR	PROSITE; PS02029; HSP70-1; FALSE_NEG.			
DR	Chaperone; Endoplasmic reticulum; Glycoprotein; Signal; ATP-binding SIGNAL			
Qy	668	OGLPEGSYSLYKETDSBGKYKVRUNSEVANATVSKTGTTSDETLAENKEPVPTGVQD	727	727
Db	1134	--ESGNIVLKKPLDRTYKLEMAQDKGYPPLSRREVQIDVDRANN---PPWDH	1185	1185
Qy	728	KINGYAL-----IVTAGISIGGWTGTTIR 754		
Db	1186	TWYGPITYKENVMPVGKRVVSKASSIEGNGPWFYR 1221		

Query Match 3.3%; Score 130.5; DB 1; Length 908; Best Local Similarity 19.3%; Pred. No. 5.4; Matches 166; Conservative 103; Mismatches 264; Indels 327; Gaps 43; Query 52 GLVSVSTPWNAPSSS----EYRWYGEYESYVG----N-LINKED (GLCNAC. . .) (POTENTIAL). Db 241 GSIRAMFSITLQPDPTQPTVIEEGYGPNPHGAKFTMDISLLENKLETHPAIR----N-LINKED (GLCNAC. . .) (POTENTIAL). Qy 149 DELNQKLRAYMVNYPHQNANGIMGGLPELNAIRYTOEAWYVYSDNAPISNPDESFKKRESE 208 349 QEEFEFI----ADSLDLYKPINP-AVTKQ-FGGYGTNP----E 383 Db 209 SNLV----STSOLSLMRQALKDPLNATKMPKQVDPDFOLSTFESEDKGDKYNGKYN 264 Db 384 INGYVILLAGSSRITIVQDOLQKLYSEE----KVLRNNAED-ESAYNGVVMRGIKLNSNFE- 438 Qy 265 LLGGGLVPLPKPTCPDPMP----PNQPOQTSVLRKVAIGDYSKLEGATQLTQDGN 318 Db 439 -----TKPLNVTDSRNTYFSRKLNSELYVTFRGSAPNKTSLNTT----DS 485 Db 319 V-NSEBQARVFSSNDIGERFLSDGTYTLELNSPAGYSAEPITFKVEAGVYTIID----374 Db 486 IPNNFTIDLFENGKLETFITIVNSGAIKNSYSSDKCSSGAVAYNITFLSSDRLSIIQEVNC 545 Qy 375 -----GKOTENPNK----E-VEPVYSEAVNDFEERSVLT'NQYKYYAK 415 Db 546 ICQSBNDIGNSQTKRNGSRLAFTSEEDVEKRLSPRSERSRLHEHKKLQDKERKFQOE 605 Qy 416 NKNGSSQVVCNFNADLKSPPDSEOGKTMPPDFTGEGVYTHIAGRDLKTYVKPRDTP 475 Db 606 NLNVLVEISNLYDARNLIMDDEVMONGPKSVEELS-EMVYVLDWLEDAFP----DTDP 658 Db 719 FETERADTIVREEEFKKIK----QPAYVSKALSTWEETLTSKNSISIEKFL 768 Qy 569 PNNNKYQSLIGTQWHPEDLYI----IRMEDKEVLPVTHNLTTRKTVTGLAGDRT 620 Db 769 AKN----LFGEDLR-EHLEIQLQFDMYRKTLEEKRLRKL----SGDES 808 Qy 621 -----KDFRF-EIENNNKQELLSTV-----KTDKTNLEFKRGKATI-NKHGES 664 Db 809 RLNEIKKLHLRNFRNLFQKKEKLKRKEQKSRRNNNETESTVINSADDKTIIVNDKTES 868

RESULT 13 DPOL-BORBU ID DPOL-BORBU STANDARD: PRT: 908 AA. AC 051498; AC 30-MAY-2000 (Rel. 39, Created) DT 30-MAY-2000 (Rel. 39, Last sequence update) DT 30-MAY-2000 (Rel. 39, Last annotation update) DE DNA POLYMERASE I (EC 2.7.7.7) (POL I). GN POLA OR BB0548.

Query Match 3.3%; Score 130.5; DB 1; Length 881; Best Local Similarity 18.3%; Pred. No. 5.1; Matches 132; Conservative 119; Mismatches 270; Indels 199; Gaps 32; Query 89 RVADLDRIVNLEGRSYQVCFNLKKAFPLGSDSSVKKWYKKHDGISTKFDYAMSPRTG 148 299 -TDELHAMPKALKATINQAAEAKLILSANSEAS----NIELSLINDIFRTSFR 348 Qy 149 DELNQKLRAYMVNYPHQNANGIMGGLPELNAIRYTOEAWYVYSDNAPISNPDESFKKRESE 208 349 QEEFEFI----ADSLDLYKPINP-AVTKQ-FGGYGTNP----E 383 Db 209 SNLV----STSOLSLMRQALKDPLNATKMPKQVDPDFOLSTFESEDKGDKYNGKYN 264 Db 384 INGYVILLAGSSRITIVQDOLQKLYSEE----KVLRNNAED-ESAYNGVVMRGIKLNSNFE- 438 Qy 265 LLGGGLVPLPKPTCPDPMP----PNQPOQTSVLRKVAIGDYSKLEGATQLTQDGN 318 Db 439 -----TKPLNVTDSRNTYFSRKLNSELYVTFRGSAPNKTSLNTT----DS 485 Db 319 V-NSEBQARVFSSNDIGERFLSDGTYTLELNSPAGYSAEPITFKVEAGVYTIID----374 Db 486 IPNNFTIDLFENGKLETFITIVNSGAIKNSYSSDKCSSGAVAYNITFLSSDRLSIIQEVNC 545 Qy 375 -----GKOTENPNK----E-VEPVYSEAVNDFEERSVLT'NQYKYYAK 415 Db 546 ICQSBNDIGNSQTKRNGSRLAFTSEEDVEKRLSPRSERSRLHEHKKLQDKERKFQOE 605 Qy 416 NKNGSSQVVCNFNADLKSPPDSEOGKTMPPDFTGEGVYTHIAGRDLKTYVKPRDTP 475 Db 606 NLNVLVEISNLYDARNLIMDDEVMONGPKSVEELS-EMVYVLDWLEDAFP----DTDP 658 Db 719 FETERADTIVREEEFKKIK----QPAYVSKALSTWEETLTSKNSISIEKFL 768 Qy 569 PNNNKYQSLIGTQWHPEDLYI----IRMEDKEVLPVTHNLTTRKTVTGLAGDRT 620 Db 769 AKN----LFGEDLR-EHLEIQLQFDMYRKTLEEKRLRKL----SGDES 808 Qy 621 -----KDFRF-EIENNNKQELLSTV-----KTDKTNLEFKRGKATI-NKHGES 664 Db 809 RLNEIKKLHLRNFRNLFQKKEKLKRKEQKSRRNNNETESTVINSADDKTIIVNDKTES 868

Query Match 3.3%; Score 130.5; DB 1; Length 908; Best Local Similarity 19.3%; Pred. No. 5.4; Matches 166; Conservative 103; Mismatches 264; Indels 327; Gaps 43; Query 13 LNTQRLVLSKNSKRENTVLYGVLFMLFALFTSMQAKTVGGLVSESTPWNINPSSSEYRW 72 Db 26 LNTQ----GENVNAF----IGFF-----KTLFLIKERNPEHLITFDSEVPT 65 Qy 73 YGYESVGRGPIYKOF-----VAHDILRN-----VADILRN----- 938 Db 66 FRKQY----PSYKATRDLPPDLPQIGWIKEGILLKAKIPFEMEGYRADDLASFARK 121 Qy 99 EGSRSYOVVCNFN-----LKKAPLPGSDSSV--KWWKKHDGT-STKFDYAM 143 Db 122 AKANNITYLISPKDQLQTMSEYKILTIENNSIEMONEVYVTKKFGINSFQIKDYL-- 179 Qy 144 PRITDELNQKLRAYMVNYPHQNANGIMGGLPELNAIRYTOEAWV 188 Db 180 -AVGDR-SDNIPGIGKAGAANLREFKTDIYGSNLEINNKHRELLIKEKNAFL 237

SEQUENCE FROM N.A. STRAIN=AVCC 35210 / B31; MEDLINE=98065943; PubMed=9433685; RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A., RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M., RA Dougherty B., Tomb J.-F., Reischmann R.D., Richardson D., Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M., RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J., RA Utterback T., Watthieu L., McDonald L., Artiach P., Bowman C., RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B., RA Smith H.O., Venter J.C.; RT "Genomic sequence of a Lyme disease spirochaete, *Borrelia burgdorferi*"; RL Nature 390:580-586(1997). - FUNCTION: IN ADDITION TO POLYMERASE ACTIVITY, THIS DNA POLYMERASE EXHIBITS 3', TO 5', AND 5', TO 3', EXONUCLEASE ACTIVITY (BY SIMILARITY). - CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE = N PYROPHOSPHATE + DNA(N) - SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-A FAMILY. - This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch). ----- CC EMBL: AE001156; AAC66909.1; - DR InterPro: IPR001098; - DR InterPro: IPR002421; - DR InterPro: IPR002562; - DR Pfam: PF01612; 3_5_exonuclease; 1. DR Pfam: PF01367; 5_3_exonuclease; 1. DR Pfam: PF00476; DNA_POL_A; 1. DR PRINTS: PR00868; DNAPOLI. DR InterPro: IPR002298; - DR InterPro: IPR002421; - DR InterPro: IPR002562; - DR Pfam: PF01612; 3_5_exonuclease; 1. DR Pfam: PF00476; DNA_POL_A; 1. DR PRINTS: PR00868; DNAPOLI. PROSITE: PS00447; DNA POLYMERASE A; 1. KW Transferase; DNA-directed DNA Polymerase; DNA replication; DNA repair; KW Hydrolase; Exonuclease; DNA-binding. FT DOMAIN 319 318 3'-5' EXONUCLEASE. DOMAIN 532 908 POLYMERASE. FT DOMAIN 532 908 POLYMERASE. SQ SEQUENCE 908 AA; 105503 MW; B88512AEB0DCBD94 CRC64;

Query Match 3.3%; Score 130.5; DB 1; Length 908; Best Local Similarity 19.3%; Pred. No. 5.4; Matches 166; Conservative 103; Mismatches 264; Indels 327; Gaps 43; Query 13 LNTQRLVLSKNSKRENTVLYGVLFMLFALFTSMQAKTVGGLVSESTPWNINPSSSEYRW 72 Db 26 LNTQ----GENVNAF----IGFF-----KTLFLIKERNPEHLITFDSEVPT 65 Qy 73 YGYESVGRGPIYKOF-----VAHDILRN-----VADILRN----- 938 Db 66 FRKQY----PSYKATRDLPPDLPQIGWIKEGILLKAKIPFEMEGYRADDLASFARK 121 Qy 99 EGSRSYOVVCNFN-----LKKAPLPGSDSSV--KWWKKHDGT-STKFDYAM 143 Db 122 AKANNITYLISPKDQLQTMSEYKILTIENNSIEMONEVYVTKKFGINSFQIKDYL-- 179 Qy 144 PRITDELNQKLRAYMVNYPHQNANGIMGGLPELNAIRYTOEAWV 188 Db 180 -AVGDR-SDNIPGIGKAGAANLREFKTDIYGSNLEINNKHRELLIKEKNAFL 237

OS Borrelia burgdorferi (Lyme disease spirochete). OC Bacterii, Spirochaetales; *Borrelia*. OC NCBI-TAXID=139; RN [1] SEQUENCE FROM N.A. STRAIN=AVCC 35210 / B31; MEDLINE=98065943; PubMed=9433685; RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A., RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M., RA Dougherty B., Tomb J.-F., Reischmann R.D., Richardson D., Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M., RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J., RA Utterback T., Watthieu L., McDonald L., Artiach P., Bowman C., RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B., RA Smith H.O., Venter J.C.; RT "Genomic sequence of a Lyme disease spirochaete, *Borrelia burgdorferi*"; RL Nature 390:580-586(1997). - FUNCTION: IN ADDITION TO POLYMERASE ACTIVITY, THIS DNA POLYMERASE EXHIBITS 3', TO 5', AND 5', EXONUCLEASE ACTIVITY (BY SIMILARITY). - CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE = N PYROPHOSPHATE + DNA(N) - SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-A FAMILY. - This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch). ----- CC EMBL: AE001156; AAC66909.1; - DR InterPro: IPR001098; - DR InterPro: IPR002421; - DR InterPro: IPR002562; - DR Pfam: PF01612; 3_5_exonuclease; 1. DR Pfam: PF01367; 5_3_exonuclease; 1. DR Pfam: PF00476; DNA_POL_A; 1. DR PRINTS: PR00868; DNAPOLI. PROSITE: PS00447; DNA POLYMERASE A; 1. KW Transferase; DNA-directed DNA Polymerase; DNA replication; DNA repair; KW Hydrolase; Exonuclease; DNA-binding. FT DOMAIN 319 318 3'-5' EXONUCLEASE. DOMAIN 532 908 POLYMERASE. FT DOMAIN 532 908 POLYMERASE. SQ SEQUENCE 908 AA; 105503 MW; B88512AEB0DCBD94 CRC64;

Db 238 SYELVLSLEENLKIPEIENFALKNFSESEIISLFEKHIAIALKTYKRDIL-----RQEKE 291
 QY 240 VPDFFOLSIFFSEDKDKYNGKQYQNLISLGGVLPTKPTPGDPPMPNQPOQTSVLRKYA 299
 Db 292 NAD--QKSURQE-----PTINSL----- 308
 QY 300 IGDYSKILEGATLQHGDNNSFOARVFSSNDIGERIELSDGTYLU-----TELNS 350
 Db 309 -----DDINTDPTENVKRSTITRKEELDLIESKKAKYVISDFTSS 351
 QY 351 PAGYS--IARPIEK-----VER-A-GAVYTLIDGKQTEMPEKEIVEYSEWYD-F 397
 QY 398 EEFSVIITONVAKFYAKKNKGSSQVYCNAIDLKSPPDSDGGKWTMPDF--TGEVK 454
 Db 399 ESNPKIGQW-KFVKILRNG-----FN--FPIPYFD---TMIAKLIDNSKV 443
 QY 455 YTHIAGRDLFKVYKVRDTPDTLKHKKVIEKGREKQSAIEYSGLTERQLRATOLA 514
 Db 444 LDFFLAKRYLHMHNKED-----VIKNDNFNANTSLEMATSYSSEDDADTFL 491
 QY 515 IYFTESSAELD-DKDKYDGFMDNSTLAVAKLIVEYAD----- 555
 Db 492 ENIETKIKLKEKDLDL-----HEIEMPNKVYIEMENGTYLDKEYLKEYGKELGK 543
 QY 556 -----SNPPQJTD-----LDFFIPNNNKYQSLIGTQWHPELDVII 591
 Db 544 ELEATNEELKSIGIDFNLNSPKHOMIEILFERNLKLPERAK-----KUDSTIK 592
 QY 592 RMEDEKKEVIVPVTNHLTKTWTGLAGDRTDFEELKNNKQELSQVTQDKUNLEFK 651
 Db 593 VLESIKEHESIENLKYRQIAKLSKTYTDNL--ELIN-----YKTNRHTSEI 640
 QY 652 DCKATINLKHQESLTLQGLPGSIVKVKW-KNSQEANATISK----- 702
 Db 641 OTKTATGRTISINPNQNTP-----IK--DEKGKIRKAFFPKPENGNTISADSQIELA 692
 QY 703 --TGTSDETL--AFFNKE 718
 Db 693 ILAHISQDEVLIKAFFNKD 712

RESULT 14

HPG_HELPJ STANDARD; PRT; 621 AA.

ID HPG_HELPJ STANDARD; PRT; 621 AA.

AC Q9ZMM2; 1

DT 01-OCT-2000 (Rel. 40. Created)
 DT 01-OCT-2000 (Rel. 40. Last sequence update)

DE HEAT SHOCK PROTEIN HPG (HIGH TEMPERATURE PROTEIN G).

GN HPG OR JH0196.

OS Helicobacter pylori J99 (Campylobacter pylori J99);
 Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
 NCBI_TaxId:85963; [1]

RP SEQUENCE FROM N A.

RX MEDLINE:9923682; PubMed:9923682;
 RA Alm R.A., Ling L.-S.M., Moir D.T., King B.L., Brown E.D., Doig P.C.,
 RA Smith D.R., Noonan B., Guild B.C., de Jonge B.L., Carmel G.,
 RA Tummolo P.J., Caruso A., Uria-Nickeisen M., Mills D.M., Ives C.,
 RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
 RA Trust T.J.;
 RT "Genomic sequence comparison of two unrelated isolates of the human
 gastric pathogen Helicobacter pylori.";
 RL Nature 397:176-180(1999).

CC -I- FUNCTION: MOLECULAR CHAPERONE. HAS ATPASE ACTIVITY
 CC (BY SIMILARITY).
 CC -I- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 90 FAMILY.

CC 01-OCT-1996 (Rel. 34, Last sequence update)
 CC 01-OCT-1996 (Rel. 36, Last sequence update)

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 CC or send an email to license@isb-sib.ch).

DR EMBL; AE001458; AAD05780; 1;
 DR P07900; 1YER;
 DR InterPro; IPR001404;
 DR Pfam; PF00183; HSP90; 2;
 DR PRINTS; PR0075; HEATSHOCK90;
 DR PROSITE; PS00295; HSP90; 1;
 KW Chaperone; ATP-binding; Heat shock;
 SQ SEQUENCE 621 AA; 7140 MW; 3CA62ABDD9796B69 CRC64;

Query Match 3.38; Score 130; DB 1; Length 621;
 Best Local Similarity 20.8%; Pred. No. 3.3; Gaps 27;
 Matches 126; Conservative 78; Mismatches 225; Indels 178;

QY 201 ESKRESESN---LVTSTQSLISMRQALKQDLPNLTAKMPQVDPDFQTSFESEDKG- 255
 Db 28 EFLRELISNASDALKNLYMLTDEKL---GNTTPSILSDSOKTLLTKDNGI 82
 QY 256 --DKYN-----KYNQNLISGLGGLVPTKPPTPGDPMPMPQPOQTSVLRKYA 300
 Db 83 GMDKSLDLIEHGTIAKS GTKSFSLASLG-----DKKKDQALIGQFGV 124
 QY 301 GDSKLEGATLQITGDNVNSEQARFSSN---DIGERIELSDGTYLTLENSPAF- 354
 Db 125 GFYSAFENVASKIIVWQVKVTHQAYAWVSDGKFEISECVKKEQDGTEITLFLKEEDSHF 184
 QY 355 -----SIAEPTFKEVAGKVTIIDQKQIENPKETVEPVSVEAYNDFEE-- 400
 Db 185 ASRWEIDSVWVKKYSEIIPPFELITYDITKFG -- EGDNKKKEVKEKCQDQINQASLWK 241
 QY 401 --SVLTQVYAKFYAKKNKGSSQVYCFNAIDLKSPPDSEDGKWTMPDFETTGKTHI 458
 Db 242 NRSELKEKDYQFVQSFADHNSPELSPVYIHKN-----VEGSLEYTL 282
 QY 459 -----AGRDKY-----YTVPRDPE-----TELKHKVIERG-----YRE 492
 Db 283 FYIPSKAPFDLFRDVYKSGVVKVYKVFITDDKELLPSYLFRVKVQGVIDSEDLPLVNSR 342
 QY 493 KQOAEIYSGLATEQTLRATOLAIYVFTSDEAELDKDQLKDYHGGMDNSTLAVAKLVE- 551
 Db 343 --LQONQKLNANISASVKKI--LSEIENSKDN-KNYKIEY-----PGKVKLEG 389
 QY 552 -YAOSENPPQJTDLFIPNNNKYQSLIGTQWHPELDVII-----KDKTNELEFKOGKAT 610
 Db 390 LKGDFENKEKILE-----LRYSKDKGEWISKEYKENLKEN---OK 429
 QY 611 TVTGLADRTDFEELKNNQE-----LLSQIV-----KDKTNELEFKOGKAT 656
 Db 430 SIYVLAGENLDDIKLAKASPLLEKAQGKQYDVLISLSDDEDAFVMGFGVNYDFT--PERDA-- 484
 QY 657 INLKHGKESLTLQGLPE-----GYSVLKETDSEGYKVVKVNSQEANATVSKTGTSDE 709
 Db 485 --SHSISKEGLGAIHDEVQDFKDLIKE-EUKDEKKGWEISHTS2AVALIGE 540
 QY 710 TIAFEN 716
 Db 541 PNMAMAN 547

RESULT 15

FUS1_SCPO STANDARD; PRT; 1372 AA.

ID FUS1_SCPO STANDARD; PRT; 1372 AA.

AC Q10719; 1

DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 36, Last sequence update)

